

09/762194

SEQUENCE LISTING

<110> Elbaz, Nathalie
Nahmias, Clara
Strosberg, Arthur Donny

<120> NUCLEIC SEQUENCES ENCODING AN AT2
RECEPTOR-INTERACTING PROTEIN (ATIP) AND THEIR APPLICATIONS

<130> 33339/208804

<140> US 09/762,194
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<150> PCT/FR99/01908
<151> 1999-08-02

<150> FR 98/09997
<151> 1998-08-04

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<170> FastSEQ for Windows Version 4.0

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tgatggtccc tggaaaagct gcttccctg cgaagttctc ccactggctt cgaagac atg 180
Met
1

ctg ttg tct ccc aaa ttc tcc tta tcc acc atc cac gtc cgc cta acc 228
Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu Thr
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gcc aaa gga ctg ctt cga aac ctc cgg ctt cct tcg ggg ctc agg aaa 276
Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg Lys
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aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat ccc 324
Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn Pro

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Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser Ser			
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gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc caa			420
Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser Gln			
70	75	80	
agt gga ttc atc ctg cac ctc agg cag ctt ctt tcc cgt ggt aac aac			468
Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn Asn			
85	90	95	
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Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg			
100	105	110	
gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc agc			564
Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Ser			
115	120	125	
ctc cgg gga gag cta gtt gct gct tca agc gcc tgt gag aag cta gaa			612
Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu Glu			
130	135	140	145
aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag aaa			660
Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln Lys			
150	155	160	
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Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu			
165	170	175	
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Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile			
180	185	190	
gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac aac			804
Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn			
195	200	205	
tta aac gcc gcc cat gag acc act aag ctt gag att gaa gct agc cac			852
Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His			
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Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser			
230	235	240	
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Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu			
245	250	255	

ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg aag	996
Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys	
260 265 270	
agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa aag	1044
Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln Lys	
275 280 285	
caa ctg tca aga gag aag gcg aat tcc aaa aac cct cag gtc atg tat	1092
Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met Tyr	
290 295 300 305	
ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag aat	1140
Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn	
310 315 320	
gag aag ctg cac cag cag gac atg aag cta atg aag atg gaa aag ctg	1188
Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys Leu	
325 330 335	
gtg gac aat aac aca gca ttg gtt gac aag ctg aag cga ttc cag cag	1236
Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln	
340 345 350	
gaa aac gag gag tta aaa gct cgc atg gac aaa cac atg gca att tca	1284
Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser	
355 360 365	
agg caa ctt tcc acc gag cag gcc gcg ctg caa gag tcc ctt gag aag	1332
Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu Lys	
370 375 380 385	
gag tca aag gtc aac aag aga ctg tcc atg gag aac gag gaa ctt ctg	1380
Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu	
390 395 400	
tgg aaa ctg cac aac gga gac ctg tgc agc ccc aag aga tcc ccc acc	1428
Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr	
405 410 415	
tcc tcg gcc atc cct ttc cag tcc ccc agg aat tct ggt tcc ttc tcc	1476
Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe Ser	
420 425 430	
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Ser Pro Ser Ile Ser Pro Arg *	
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ctctctggaa tatccccagg atatcggag agcagccgcc aaccgtatca gctacgtacg	1650
aatagagagc tccaatagaa gacttttaac ttggtccaaa agcctcctcc aaaaacagat	1710
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1803

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 Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn
 35 40 45
 Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
 50 55 60
 Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
 65 70 75 80
 Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
 85 90 95
 Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
 100 105 110
 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
 115 120 125
 Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
 130 135 140
 Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
 145 150 155 160
 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
 165 170 175
 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
 180 185 190
 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
 195 200 205
 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
 210 215 220
 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
 225 230 235 240
 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
 245 250 255
 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
 260 265 270
 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
 275 280 285
 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
 290 295 300
 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
 305 310 315 320
 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
 325 330 335
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 340 345 350
 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile

355	360	365
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370	375	380
Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu		
385	390	395
Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro		400
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aaa aac act gtc att ttc cac aca gtt gaa aag ggc agg cag aag aat Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn 35 40 45	144
ccc agg agc ctg tgc atc cag acc cag aca gct cca gat gtg ctg tcc Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser 50 55 60	192
tcc gag aga acg ctt gag ttg gcc caa tac aag aca aaa tgt gaa agc Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser 65 70 75 80	240
caa agt gga ttc atc ctg cac ctc agg cag ctt ctt tcc cgt ggt aac Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn 85 90 95	288
aac aag ttt gaa gcg ctg aca gtt gtg atc cag cac ctc ctg tct gag Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu 100 105 110	336
cgg gag gaa gca ctg aag caa cac aaa acc ctc tct caa gaa ctt gtc Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val 115 120 125	384

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130 135 140	
gaa aag gct agg gct gac tta cag aca gcg tat caa gaa ttt gtc cag	480
Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln	
145 150 155 160	
aaa cta aac cag cag cat cag aca gac cgg acg gaa ctg gag aac cgg	528
Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg	
165 170 175	
ctg aag gac tta tac acc gca gag tgt gag aag ctt cag agc att tac	576
Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr	
180 185 190	
att gag gag gca gaa aaa tat aaa act caa ctg caa gag cag ttt gac	624
Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp	
195 200 205	
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Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser	
210 215 220	
cac tcg gag aag gtg gaa ttg ctg aag aag acc tat gaa acc tcc ctt	720
His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu	
225 230 235 240	
tca gaa atc aag aag agc cat gag atg gag aag aag tca ctg gag gat	768
Ser Glu Ile Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp	
245 250 255	
ctg ctt aat gag aag cag gaa tcg ctg gag aaa caa atc aat gat ctg	816
Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu	
260 265 270	
aag agt gaa aac gat gct tta aac gaa agg ttg aaa tca gag gag caa	864
Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln	
275 280 285	
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Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met	
290 295 300	
tat ctg gag caa gaa cta gaa agc ctg aag gct gtg tta gag atc aag	960
Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys	
305 310 315 320	
aat gag aag ctg cac cag cag gac atg aag cta atg aag atg gaa aag	1008
Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys	
325 330 335	

ctg gtg gac aat aac aca gca ttg gtt gac aag ctg aag cga ttc cag	1056
Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln	
340 345 350	
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Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile	
355 360 365	
tca agg caa ctt tcc acc gag cag gcc gcg ctg caa gag tcc ctt gag	1152
Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu	
370 375 380	
aag gag tca aag gtc aac aag aga ctg tcc atg gag aac gag gaa ctt	1200
Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu	
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 35 40 45
 Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser
 50 55 60
 Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser
 65 70 75 80
 Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn
 85 90 95
 Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu
 100 105 110
 Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val
 115 120 125
 Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu
 130 135 140

Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
 145 150 155 160
 Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
 165 170 175
 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
 180 185 190
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 195 200 205
 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
 210 215 220
 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
 225 230 235 240
 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
 245 250 255
 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
 260 265 270
 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
 275 280 285
 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
 290 295 300
 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
 305 310 315 320
 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
 325 330 335
 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
 340 345 350
 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
 355 360 365
 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
 370 375 380
 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
 385 390 395 400
 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
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 musculus foetal cDNA library

 <223> Insert identified by two-hybrid screening of a M.
 musculus foetal cDNA library

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acc gca gag tgt gag aag ctt cag agc att tac att gag gag gca gaa 96
 Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu
 20 25 30

aaa tat aaa actcaa ctg caa gag cag ttt gac aac tta aac gcc gcc 144
 Lys Tyr Lys Thr Gln Leu Gln Glu Phe Asp Asn Leu Asn Ala Ala
 35 40 45

cat gag acc act aag ctt gag att gaa gct agc cac tcg gag aag gtg 192
 His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val
 50 55 60

gaa ttg ctg aag aag acc tat gaa acc tcc ctt tca gaa atc aag aag 240
 Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys
 65 70 75 80

agc cat gag atg gag aag aag tca ctg gag gat ctg ctt aat gag aag 288
 Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys
 85 90 95

cag gaa tcg ctg gag aaa caa atc aat gat ctg aag agt gaa aac gat 336
 Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp
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 Ala Leu Asn Glu Arg Leu
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<211> 118

<212> PRT

<213> Artificial Sequence

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<223> Insert identified by yeast two hybrid screening of
 a M. musculus fetal cDNA library

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 20 25 30
 Lys Tyr Lys Thr Gln Leu Gln Glu Phe Asp Asn Leu Asn Ala Ala
 35 40 45
 His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val
 50 55 60
 Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys

65	70	75	80
Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys			
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Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp			
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<213> Homo sapiens

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<221> CDS

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cctggggat tttttcttc tatgcctctg tggtgaatg acatttgcgt tgtaggcata	180
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cagtccatgg aaattgcctc ttctgtaaa tctgccacc tgctccgaag ac atg ttg	298
Met Leu	
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ttg tct ccc aaa ttc tcc tta tcc acc att cac ata cga ctg acg gcc	346
Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Ile Arg Leu Thr Ala	
5 10 15	

aaa gga ttg ctt cga aac ctt cga ctt cct tca ggg ttt agg aga agc	394
Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg Arg Ser	
20 25 30	

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Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn Pro Arg	
35 40 45 50	

agc tta tgt atc cag cca cag aca gct ccc gat gcg ctg ccc cct gag	490
Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro Pro Glu	
55 60 65	

aaa aca ctt gaa ttg acg caa tat aaa aca aaa tgt gaa aac caa agt	538
Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn Gln Ser	
70 75 80	

gga ttt atc ctg cag ctc aag cag ctt ctt gcc tgt ggt aat acc aag	586
Gly Phe Ile Leu Gln Leu Lys Gln Leu Ala Cys Gly Asn Thr Lys	
85 90 95	

ttt gag gca ttg aca gtt gtg att cag cac ctg ctg tct gag cgg gag	634
Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu Arg Glu	
100 105 110	

gaa gca ctg aaa caa cac aaa acc cta tct caa gaa ctt gtt aac ctc	682
Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Asn Leu	
115 120 125 130	
cgg gga gag cta gtc act gct tca acc acc tgt gag aaa tta gaa aaa	730
Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu Glu Lys	
135 140 145	
gcc agg aat gag tta caa aca gtg tat gaa gca ttc gtc cag cag cac	778
Ala Arg Asn Glu Leu Gln Thr Val Tyr Glu Ala Phe Val Gln Gln His	
150 155 160	
cag gct gaa aaa aca gaa cga gag aat cgg ctt aaa gag ttt tac acc	826
Gln Ala Glu Lys Thr Glu Arg Glu Asn Arg Leu Lys Glu Phe Tyr Thr	
165 170 175	
agg gag tat gaa aag ctt cgg gac act tac att gaa gaa gca gag aag	874
Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala Glu Lys	
180 185 190	
tac aaa atg caa ttg caa gag cag ttt gac aac tta aat gcg cat gaa	922
Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala His Glu	
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acc tct aag ttg gaa att gaa gct agc cac tca gag aaa ctt gaa ttg	970
Thr Ser Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Leu Glu Leu	
215 220 225	
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Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys Gly His	
230 235 240	
gaa ata gaa aag aaa tcg ctt gaa gat tta ctt tct gag aag cag gaa	1066
Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys Gln Glu	
245 250 255	
tcg cta gag aag caa atc aat gat ctg aag agt gaa aat gat gct tta	1114
Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp Ala Leu	
260 265 270	
aat gaa aaa ttg aaa tca gaa gaa caa aaa aga aga gca aga gaa aaa	1162
Asn Glu Lys Leu Lys Ser Glu Glu Gln Lys Arg Arg Ala Arg Glu Lys	
275 280 285 290	
gca aat ttg aaa aat cct cag atc atg tat cta gaa cag gag tta gaa	1210
Ala Asn Leu Lys Asn Pro Gln Ile Met Tyr Leu Glu Gln Glu Leu Glu	
295 300 305	
agc ctg aaa gct gtg tta gag atc aag aat gag aaa ctg cat caa cag	1258
Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His Gln Gln	
310 315 320	

gac atc aag tta atg aaa atg gag aaa ctg gtg gac aac aac aca gca	1306
Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn Thr Ala	
325 330 335	
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Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu Leu Lys	
340 345 350	
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Ala Arg Met Asp Lys His Met Ala Ile Ser Arg Gln Leu Ser Thr Glu	
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Gln Ala Val Leu Gln Glu Ser Leu Glu Lys Glu Ser Lys Val Asn Lys	
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atgttagttc actgcccattt	catgagatat ctctgctcac	gcttccaagt tgttctcaat	3390
gacatttagcc aaagttgggt	ttgcccattca tcccttaggc	atggtaaaatc ttgtgttgc	3450
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<212> PRT

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Pro	Arg	Ser	Leu	Cys	Ile	Gln	Pro	Gln	Thr	Ala	Pro	Asp	Ala	Leu	Pro
						50				55					60
Pro	Glu	Lys	Thr	Leu	Glu	Leu	Thr	Gln	Tyr	Lys	Thr	Lys	Cys	Glu	Asn
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Gln	Ser	Gly	Phe	Ile	Leu	Gln	Leu	Lys	Gln	Leu	Leu	Ala	Cys	Gly	Asn
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Thr	Lys	Phe	Glu	Ala	Leu	Thr	Val	Val	Ile	Gln	His	Leu	Ser	Glu	
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Arg	Glu	Glu	Ala	Leu	Lys	Gln	His	Lys	Thr	Leu	Ser	Gln	Glu	Leu	Val
						115				120					125
Asn	Leu	Arg	Gly	Glu	Leu	Val	Thr	Ala	Ser	Thr	Thr	Cys	Glu	Lys	Leu
						130				135					140
Glu	Lys	Ala	Arg	Asn	Glu	Leu	Gln	Thr	Val	Tyr	Glu	Ala	Phe	Val	Gln
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Gln	His	Gln	Ala	Glu	Lys	Thr	Glu	Arg	Glu	Asn	Arg	Leu	Lys	Glu	Phe
						165				170					175
Tyr	Thr	Arg	Glu	Tyr	Glu	Lys	Leu	Arg	Asp	Thr	Tyr	Ile	Glu	Glu	Ala
						180				185					190
Glu	Lys	Tyr	Lys	Met	Gln	Leu	Gln	Gln	Phe	Asp	Asn	Leu	Asn	Ala	
						195				200					205
His	Glu	Thr	Ser	Lys	Leu	Glu	Ile	Glu	Ala	Ser	His	Ser	Glu	Lys	Leu
						210				215					220
Glu	Leu	Leu	Lys	Lys	Ala	Tyr	Glu	Ala	Ser	Leu	Ser	Glu	Ile	Lys	Lys
						225				230					240
Gly	His	Glu	Ile	Glu	Lys	Lys	Ser	Leu	Glu	Asp	Leu	Leu	Ser	Glu	Lys
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 Glu Lys Ala Asn Leu Lys Asn Pro Gln Ile Met Tyr Leu Glu Gln Glu
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 Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His
 305 310 315 320
 Gln Gln Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn
 325 330 335
 Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Glu Asn Glu Glu
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 370 375 380
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 385 390 395 400
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 Ser Pro Arg
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 Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg
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 aga agc act gtt ttc cac aca gtt gaa aag agc agg caa aag aat 144
 Arg Ser Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn
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 cct cga agc tta tgt atc cag cca cag aca gct ccc gat gcg ctg ccc 192
 Pro Arg Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro
 50 55 60

 cct gag aaa aca ctt gaa ttg acg caa tat aaa aca aaa tgt gaa aac 240
 Pro Glu Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn

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caa agt gga ttt atc ctg cag ctc aag cag ctt ctt gcc tgt ggt aat				288
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85	90	95		
acc aag ttt gag gca ttg aca gtt gtg att cag cac ctg ctg tct gag				336
Thr Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu				
100	105	110		
cgg gag gaa gca ctg aaa caa cac aaa acc cta tct caa gaa ctt gtt				384
Arg Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val				
115	120	125		
aac ctc cgg gga gag cta gtc act gct tca acc acc tgt gag aaa tta				432
Asn Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu				
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145	150	155	160	
cag cac cag gct gaa aaa aca gaa cga gag aat cgg ctt aaa gag ttt				528
Gln His Gln Ala Glu Lys Thr Glu Arg Glu Asn Arg Leu Lys Glu Phe				
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Tyr Thr Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala				
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Glu Lys Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala				
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Glu Leu Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys				
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ggc cat gaa ata gaa aag aaa tcg ctt gaa gat tta ctt tct gag aag				768
Gly His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys				
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Ala Leu Asn Glu Lys Leu Lys Ser Glu Glu Gln Lys Arg Arg Ala Arg				
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Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu			
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Asp	Ala	Leu
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Thr	Leu	Glu
Leu	Thr	Gln
Tyr	Lys	Thr
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Asn		
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Gln	Leu	Lys
Gln	Leu	Leu
Ala	Cys	Gly
Asn		
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Thr	Val	Val
Ile	Gln	His
Leu	Leu	Ser
Glu		
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Gln	His	Lys
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Gln	Glu	Leu
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Glu	Tyr	Glu
Lys	Leu	Arg
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Ile	Glu	Glu
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Tyr	Lys	Met
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Gln	Glu	Gln
Phe	Asp	Asn
Asn	Leu	Asn
Ala		
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His	Glu	Thr
Ser	Lys	Leu
Glu	Ile	Glu
Ala	Ser	His
His	Ser	Glu
Glu	Lys	Leu
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Leu	Lys	Ala
Tyr	Glu	Ala
Ser	Leu	Ser
Glu	Ile	Glu
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Ile	Glu	Lys
Lys	Ser	Leu
Glu	Asp	Leu
Asp	Leu	Ser
Glu	Lys	Glu
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Leu	Glu	Lys
Gln	Ile	Asn
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Glu	Lys	Leu
Lys	Ser	Glu
Glu	Gln	Lys
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Met	Lys	Met
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Asp	Leu	Val
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Lys	His	Met
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Ser	Gly	Ser
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34

Rec'd PCT/PTO 19 APR 2001

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(B) STREET: 66 rue de Javel
(C) CITY: Paris
(E) COUNTRY: FRANCE
(F) POSTAL CODE: 75015

(ii) TITLE OF THE INVENTION: NUCLEIC SEQUENCES ENCODING AN AT2 RECEPTOR-INTERACTING PROTEIN (ATIP) AND THEIR APPLICATIONS

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1803 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 178..1500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TGATGGTCCC	TGGAAAAGCT	GCTTCCCCTG	CGAAGTTCTC	CCACTGGCTT	CGAAGAC	177
ATG CTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATC CAC GTC CGC CTA						225
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ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT CCT TCG GGG CTC AGG						273
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg						
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Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn						
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CAC TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu 225 230 235 240	897
TCA GAA ATC AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT Ser Glu Ile Lys Ser His Glu Met Glu Lys Ser Leu Glu Asp 245 250 255	945
CTG CTT AAT GAG AAG CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu 260 265 270	993
AAG AGT GAA AAC GAT GCT TTA AAC GAA AGG TTG AAA TCA GAG GAG CAA Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln 275 280 285	1041
AAG CAA CTG TCA AGA GAG AAG GCG AAT TCC AAA AAC CCT CAG GTC ATG Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met 290 295 300	1089
TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT GTG TTA GAG ATC AAG Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys 305 310 315 320	1137
AAT GAG AAG CTG CAC CAG CAG GAC ATG AAG CTA ATG AAG ATG GAA AAG Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys 325 330 335	1185
CTG GTG GAC AAT AAC ACA GCA TTG GTT GAC AAG CTG AAG CGA TTC CAG Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln 340 345 350	1233
CAG GAA AAC GAG GAG TTA AAA GCT CGC ATG GAC AAA CAC ATG GCA ATT Gln Glu Asn Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile 355 360 365	1281
TCA AGG CAA CTT TCC ACC GAG CAG GCC GCG CTG CAA GAG TCC CTT GAG Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu 370 375 380	1329
AAG GAG TCA AAG GTC AAC AAG AGA CTG TCC ATG GAG AAC GAG GAA CTT Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu 385 390 395 400	1377
CTG TGG AAA CTG CAC AAC GGA GAC CTG TGC AGC CCC AAG AGA TCC CCC Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro 405 410 415	1425

ACC TCC TCG GCC ATC CCT TTC CAG TCC CCC AGG AAT TCT GGT TCC TTC	1473
Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe	
420 425 430	
TCC AGC CCC AGC ATC TCA CCC AGA TGA CGGCTTCTGA ACGCAGGAGA	1520
Ser Ser Pro Ser Ile Ser Pro Arg *	
435 440	
CTCTCTGAAG GCACTGAGGT GCGCTTCTGC AGGACTGACC CTCTCATGGG AACTCGAGTT	1580
GCTGCGTTAG CTCTCTGGAA TATCCCCAGG ATATCGGGAG AGCAGCCGCC AACCGTATCA	1640
GCTACGTACG AATAGAGAGC TCCAATAGAA GACTTTAAC TTGGTCCAAA AGCCTCCTCC	1700
AAAAACAGAT TTCGGAAC TG AAGTGGACAT AGTTGCACAA AGCACTTACG GAACGAGGGA	1760
ACCTTGTCT TTGCCTTCCT TCACCTAAGC ATAGGCTTTC CAG	1803

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu	
1 5 10 15	
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg	
20 25 30	
Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn	
35 40 45	
Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser	
50 55 60	
Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser	
65 70 75 80	
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn	
85 90 95	
Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu	
100 105 110	
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val	
115 120 125	
Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu	
130 135 140	

Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln
145 150 155 160

Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
165 170 175

Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
180 185 190

Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
195 200 205

Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
210 215 220

His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
225 230 235 240

Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
245 250 255

Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
260 265 270

Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
275 280 285

Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
290 295 300

Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
305 310 315 320

Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
325 330 335

Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
340 345 350

Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
355 360 365

Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
370 375 380

Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
385 390 395 400

Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
405 410 415

Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
420 425 430

Ser Ser Pro Ser Ile Ser Pro Arg *
435 440

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG CTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATC CAC GTC CGC CTA	48	
Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu		
445	450	455
ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT CCT TCG GGG CTC AGG	96	
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg		
460	465	470
AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG CAG AAG AAT	144	
Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn		
CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GCT CCA GAT GTG CTG TCC	192	
Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser		
TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC	240	
Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser		
CAA AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CCT TCC CGT GGT AAC	288	
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn		
AAC AAG TTT GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG	336	
Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu		
CGG GAG GAA GCA CTG AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC	384	
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val		
AGC CTC CGG GGA GAG CTA GTT GCT GCT TCA AGC GCC TGT GAG AAG CTA	432	
Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu		
GAA AAG GCT AGG GCT GAC TTA CAG ACA GCG TAT CAA GAA TTT GTC CAG	480	
Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln		

AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACG GAA CTG GAG AAC CGG Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg	528
CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG AGC ATT TAC Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr	576
ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT GAC Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp	624
AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser	672
CAC TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu	720
TCA GAA ATC AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp	768
CTG CTT AAT GAG AAG CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu	816
AAG AGT GAA AAC GAT GCT TTA AAC GAA AGG TTG AAA TCA GAG GAG CAA Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln	864
AAG CAA CTG TCA AGA GAG AAG GCG AAT TCC AAA AAC CCT CAG GTC ATG Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met	912
TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT GTG TTA GAG ATC AAG Tyr Leu Glu Gln Glu Leu Ser Leu Lys Ala Val Leu Glu Ile Lys	960
AAT GAG AAG CTG CAC CAG CAG GAC ATG AAG CTA ATG AAG ATG GAA AAG Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys	1008
CTG GTG GAC AAT AAC ACA GCA TTG GTT GAC AAG CTG AAG CGA TTC CAG Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln	1056
CAG GAA AAC GAG GAG TTA AAA GCT CGC ATG GAC AAA CAC ATG GCA ATT Gln Glu Asn Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile	1104
TCA AGG CAA CTT TCC ACC GAG CAG GCC GCG CTG CAA GAG TCC CTT GAG Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu	1152

AAG GAG TCA AAG GTC AAC AAG AGA CTG TCC ATG GAG AAC GAG GAA CTT	1200
Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu	
CTG TGG AAA CTG CAC AAC GGA GAC CTG TGC AGC CCC AAG AGA TCC CCC	1248
Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro	
ACC TCC TCG GCC ATC CCT TTC CAG TCC CCC AGG AAT TCT GGT TCC TTC	1296
Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe	
TCC AGC CCC AGC ATC TCA CCC AGA TG A	1323
Ser Ser Pro Ser Ile Ser Pro Arg	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Val Arg Leu			
1	5	10	15
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Leu Arg			
20	25	30	
Lys Asn Thr Val Ile Phe His Thr Val Glu Lys Gly Arg Gln Lys Asn			
35	40	45	
Pro Arg Ser Leu Cys Ile Gln Thr Gln Thr Ala Pro Asp Val Leu Ser			
50	55	60	
Ser Glu Arg Thr Leu Glu Leu Ala Gln Tyr Lys Thr Lys Cys Glu Ser			
65	70	75	80
Gln Ser Gly Phe Ile Leu His Leu Arg Gln Leu Leu Ser Arg Gly Asn			
85	90	95	
Asn Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu			
100	105	110	
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val			
115	120	125	
Ser Leu Arg Gly Glu Leu Val Ala Ala Ser Ser Ala Cys Glu Lys Leu			
130	135	140	
Glu Lys Ala Arg Ala Asp Leu Gln Thr Ala Tyr Gln Glu Phe Val Gln			
145	150	155	160

Lys Leu Asn Gln Gln His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg
 165 170 175
 Leu Lys Asp Leu Tyr Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr
 180 185 190
 Ile Glu Glu Ala Glu Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp
 195 200 205
 Asn Leu Asn Ala Ala His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser
 210 215 220
 His Ser Glu Lys Val Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu
 225 230 235 240
 Ser Glu Ile Lys Lys Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp
 245 250 255
 Leu Leu Asn Glu Lys Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu
 260 265 270
 Lys Ser Glu Asn Asp Ala Leu Asn Glu Arg Leu Lys Ser Glu Glu Gln
 275 280 285
 Lys Gln Leu Ser Arg Glu Lys Ala Asn Ser Lys Asn Pro Gln Val Met
 290 295 300
 Tyr Leu Glu Gln Glu Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys
 305 310 315 320

 Asn Glu Lys Leu His Gln Gln Asp Met Lys Leu Met Lys Met Glu Lys
 325 330 335
 Leu Val Asp Asn Asn Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln
 340 345 350
 Gln Glu Asn Glu Glu Leu Lys Ala Arg Met Asp Lys His Met Ala Ile
 355 360 365
 Ser Arg Gln Leu Ser Thr Glu Gln Ala Ala Leu Gln Glu Ser Leu Glu
 370 375 380
 Lys Glu Ser Lys Val Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu
 385 390 395 400
 Leu Trp Lys Leu His Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro
 405 410 415
 Thr Ser Ser Ala Ile Pro Phe Gln Ser Pro Arg Asn Ser Gly Ser Phe
 420 425 430
 Ser Ser Pro Ser Ile Ser Pro Arg
 435 440

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CAT CAG ACA GAC CGG ACG GAA CTG GAG AAC CGG CTG AAG GAC TTA TAC	48
His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu Lys Asp Leu Tyr	
440	445
450	
ACC GCA GAG TGT GAG AAG CTT CAG AGC ATT TAC ATT GAG GAG GCA GAA	96
Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu	
455	460
465	
AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT GAC AAC TTA AAC GCC GCC	144
Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala Ala	
470	475
480	
CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC CAC TCG GAG AAG GTG	192
His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val	
485	490
495	500
GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT TCA GAA ATC AAG AAG	240
Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys	
505	510
515	
AGC CAT GAG ATG GAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG	288
Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys	
520	525
530	
CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT	336
Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp	
535	540
545	
GCT TTA AAC GAA AGG TTG	354
Ala Leu Asn Glu Arg Leu	
550	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His Gln Thr Asp Arg Thr Glu Leu Glu Asn Arg Leu Lys Asp Leu Tyr
 1 5 10 15

Thr Ala Glu Cys Glu Lys Leu Gln Ser Ile Tyr Ile Glu Glu Ala Glu
 20 25 30

Lys Tyr Lys Thr Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala Ala
 35 40 45

His Glu Thr Thr Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Val
 50 55 60

Glu Leu Leu Lys Lys Thr Tyr Glu Thr Ser Leu Ser Glu Ile Lys Lys
 65 70 75 80

Ser His Glu Met Glu Lys Lys Ser Leu Glu Asp Leu Leu Asn Glu Lys
 85 90 95

Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp
 100 105 110

Ala Leu Asn Glu Arg Leu
 115

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3742 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 293..1600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CAGTGTGATG TGGTTCAGAG GCAGCTTCTA GACCTGCAGG AGGGAGATTG TATTCAGAGG	60
AAGAGCATCA TTTTGGCAAC ATCTGAAAGT GAAAACGGAA GCCAGAAACA CTTGGCCAGC	120
CCTGGGGGAT TTTTTCTTC TATGCCTCTG TGGTGGAATG ACATTTGCTG TGTAGGCATC	180
TTTCCTCTGA CTGTATTTCT TGGCCTTGAA GAGTACTGAG TTTAAAAAGA CAGTATGTGA	240
CAGTCCATGG AAATTGCCCTC TTCTGTGAAA TCTCGCCACC TGCTCCGAAG AC ATG Met	295

TTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATT CAC ATA CGA CTG ACG Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Ile Arg Leu Thr	343
GCC AAA GGA TTG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg Arg	391
AGC ACT GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT Ser Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn Pro	439
CGA AGC TTA TGT ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CCT Arg Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro Pro	487
GAG AAA ACA CTT GAA TTG ACG CAA TAT AAA ACA AAA TGT GAA AAC CAA Glu Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn Gln	535
AGT GGA TTT ATC CTG CAG CTC AAG CAG CTT CTT GCC TGT GGT AAT ACC Ser Gly Phe Ile Leu Gln Leu Lys Gln Leu Ala Cys Gly Asn Thr	583
AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG CAC CTG CTG TCT GAG CGG Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Ser Glu Arg	631
GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA GAA CTT GTT AAC Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val Asn	679
CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA TTA GAA Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Cys Glu Lys Leu Glu	727
AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG Lys Ala Arg Asn Glu Leu Gln Thr Val Tyr Glu Ala Phe Val Gln Gln	775
CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC His Gln Ala Glu Lys Thr Glu Arg Glu Asn Arg Leu Lys Glu Phe Tyr	823
ACC AGG GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG Thr Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala Glu	871
AAG TAC AAA ATG CAA TTG CAA GAG CAG TTT GAC AAC TTA AAT GCG CAT Lys Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala His	919
GAA ACC TCT AAG TTG GAA ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA Glu Thr Ser Lys Leu Glu Ile Glu Ala Ser His Ser Glu Leu Glu	967
TTG CTA AAG AAG GCC TAT GAA GCC TCC CTT TCA GAA ATT AAG AAA GGC Leu Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys Gly	1015

CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT TTA CTT TCT GAG AAG CAG His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys Gln	1063
GAA TCG CTA GAG AAG CAA ATC AAT GAT CTG AAG AGT GAA AAT GAT GCT Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp Ala	1111
TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA AGA GAA Leu Asn Glu Lys Leu Lys Ser Glu Glu Gln Lys Arg Arg Ala Arg Glu	1159
AAA GCA AAT TTG AAA AAT CCT CAG ATC ATG TAT CTA GAA CAG GAG TTA Lys Ala Asn Leu Lys Asn Pro Gln Ile Met Tyr Leu Glu Gln Glu Leu	1207
GAA AGC CTG AAA GCT GTG TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His Gln	1255
CAG GAC ATC AAG TTA ATG AAA ATG GAG AAA CTG GTG GAC AAC AAC ACA Gln Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn Thr	1303
GCA TTG GTT GAC AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu Leu	1351
AAA GCT CGG ATG GAC AAG CAC ATG GCA ATC TCA AGG CAG CTT TCC ACG Lys Ala Arg Met Asp Lys His Met Ala Ile Ser Arg Gln Leu Ser Thr	1399
GAG CAG GCT GTT CTG CAA GAG TCG CTG GAG AAG GAG TCG AAA GTC AAC Glu Gln Ala Val Leu Gln Glu Ser Leu Glu Ser Lys Val Asn	1447
AAG CGA CTC TCT ATG GAA AAC GAG GAG CTT CTG TGG AAA CTG CAC AAT Lys Arg Leu Ser Met Glu Asn Glu Leu Leu Trp Lys Leu His Asn	1495
GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC TCC GCC ATC CCT Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr Ser Ser Ala Ile Pro	1543
TTG CAG TCA CCA AGG AAT TCG GGC TCC TTC CCT AGC CCC AGC ATT TCA Leu Gln Ser Pro Arg Asn Ser Gly Ser Phe Pro Ser Pro Ser Ile Ser	1591
CCC AGA TGA CACGTCCCCA AAGTCCACAG ACTCTCTGAA AGCATTGTA Pro Arg *	1640
TGCAGGTCTG CAGGACTGAC CCCAAGGAGG AACGTGGCA CAAGAGGTAT ATCAGCACAC	1700
GTTGTGATCAC CGTAGGTAAC TGGAGCGTCA CCACCGGCAG AATCGAGCTT CTGAGACTGG	1760

AAGTCTGGAG	GAAGACTTTT	GCCTCCGTCC	AAAAGATTCC	TCCAAAAAAA	GATTTAAAAA	1820
AAGATTCGG	CATCGACACG	GACGTTGTTG	CACAAAGCAC	TTAAAGAACG	AGAGCATCTT	1880
GTTCATTGCC	TTTTCACCT	AAGCATAAGG	GGAAAAACTC	TCAGGGCCCT	ATTAAGATTT	1940
ATAACCTTTG	TAATGTTCTT	CACCACAGAC	ACCTTCTTGT	GAGTTTCAG	TCTGACTGTG	2000
GGGGTGGGGG	GTGTGAATGA	AATGGATGTC	ACAGAGTGTC	ATGTGTCTGA	TGCAGCCTCC	2060
TCTGCTGTGT	ATTAATGTC	AAAATCTGAA	TATATCTGGA	TATGTACTAA	TCAAATAATA	2120
ATCAATCAAT	CAGCATATAC	ATTCAGCCA	AAGCCATAGA	AGAAAAAGCA	ATAGTTGCTT	2180
GAATTATGAT	CATCTACAC	CAACTCTGCT	CAGCCCTGTA	ACAGGGTAGG	GAGAGGGTAT	2240
AACAGGAAGA	GCTTGACTT	GTCCTGTCT	ATACATTCTC	TGTATCTTT	GGGGGTAACT	2300
TCTTGGCAGT	TTTCAGTGT	TCAGCCATGT	CAGTTGAAAC	TAGATTTTC	TGTAGATTTT	2360
TTACTTACCC	ATGTGAGCCT	AACACTATCC	TGTAATTCTAT	TTTCTCAGGC	TATGTGTAAA	2420
TGTAGAACCC	TAATTTTCT	ATAAAAAAAC	AAACTAACTA	ACTGTGTAAA	GAAAGAAAAA	2480
GGGAAGTACC	AATGGGTTTT	TCCACCTTAT	TTTTACCTTT	GATCTACCCT	TGCAGATTAA	2540
ACCTGTCTTC	TTCCCTCCCA	TTATTCTCAT	TTTCCTTTA	CCTTTCTCCA	CCATCCAGAG	2600
CCACAAAAGC	AAACCTTCTA	CCTCCTACCT	ACTTTCTCT	GGGACAAGGA	TAAAGGAATA	2660
TGATTTCCA	GAGCCCCAGA	GCCAGCTCAT	CTTCCAGGTG	CTGAAACCAC	TTTCCAAATA	2720
AACTAAAGCC	TGGATTGAT	ATTACAAATT	TTGGGAAATC	TTAGAATAAA	GAACGAGAAC	2780
AAGGAAGTCA	TTGGCTAGTA	TAATTAAGAA	AGGTAGGATT	CAGTGCTTAC	CGATGATGCA	2840
GTACTTGATA	GAAGAAAACA	GTCTGGGAGG	ATAGCGCTCA	TTTTTCAGTT	ACCCTTAAG	2900
GAGTCCCTTT	GTCTTGGGA	AAGTAGCAGA	ATGGTCCGCT	TCTTTCCCAT	GAGTGGAAAA	2960
TGTGGCTTGT	CCAACTCTCC	TCCAGGTTGC	ATTCAGTTT	CTTTCCAAAA	CTTATTACCT	3020
CCCCTAATCC	TGAGACTTTG	GAAAAGGTGG	AAGGAAGAAC	TGTTGCTTTA	TCTCCCCCTC	3080
CCTGCATGTG	TCAACATTGT	GATGTCAGTA	TTTACTAATC	TACATTCACT	GGCTGTACAA	3140
ATAACAGCTG	TAGTAAGAAC	AGATTCAAGGA	TGCTAGAGGT	GAATATTTGG	GTCATTACAA	3200
TGTACACTAC	ATAGCAAGTT	GATACTCATG	TTGCATGTT	TTTAAATTA	GTGATTTGT	3260
GTCTTAAGTC	TTTAACCTCC	AATACTCAT	CATGTATGTA	ACCTTCCATG	TTTGCTTCTG	3320
ATAAAATGGAA	ATGTAGGTTTC	ACTGCCACTT	CATGAGATAT	CTCTGCTCAC	GCTTCCAAGT	3380
TGTTCTCAAT	GACATTAGCC	AAAGTTGGGT	TTGCCATTCA	TCCCCTAGGC	ATGGTAAATC	3440
TTGTGTTGTT	CCCTGCTGTC	CTCCGTATTA	CGTGACCGGC	AAATAATCT	CATAGCAGTT	3500

AATATAAAAC ATCTTGAG GATGGGAGAG AACAGGAGGG AAGATGGAA ACAAAATAGA	3560
GAATTCTTAA GATTTGTTT AAACCAAATG TTTCATGTAG AATGCAAAT GTTGGCACGT	3620
CAAAAATATG AATGTGAGA CAACTGTAGT TGTGCTCAGT TTGTAGTGAT GGGAAAGTGT	3680
TTTTACTCTG ATCAAATAAA TAATGCTGGA ATACTCAAAA AAAAAAAA AAAAAAAA	3740
AA	3742

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 435 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Leu Leu Ser Pro Lys Phe Ser Leu Ser Thr Ile His Ile Arg Leu			
1	5	10	15
Thr Ala Lys Gly Leu Leu Arg Asn Leu Arg Leu Pro Ser Gly Phe Arg			
20	25	30	
Arg Ser Thr Val Val Phe His Thr Val Glu Lys Ser Arg Gln Lys Asn			
35	40	45	
Pro Arg Ser Leu Cys Ile Gln Pro Gln Thr Ala Pro Asp Ala Leu Pro			
50	55	60	
Pro Glu Lys Thr Leu Glu Leu Thr Gln Tyr Lys Thr Lys Cys Glu Asn			
65	70	75	80
Gln Ser Gly Phe Ile Leu Gln Leu Lys Gln Leu Leu Ala Cys Gly Asn			
85	90	95	
Thr Lys Phe Glu Ala Leu Thr Val Val Ile Gln His Leu Leu Ser Glu			
100	105	110	
Arg Glu Glu Ala Leu Lys Gln His Lys Thr Leu Ser Gln Glu Leu Val			
115	120	125	
Asn Leu Arg Gly Glu Leu Val Thr Ala Ser Thr Thr Cys Glu Lys Leu			
130	135	140	
Glu Lys Ala Arg Asn Glu Leu Gln Thr Val Tyr Glu Ala Phe Val Gln			
145	150	155	160
Gln His Gln Ala Glu Lys Thr Glu Arg Glu Asn Arg Leu Lys Glu Phe			
165	170	175	
Tyr Thr Arg Glu Tyr Glu Lys Leu Arg Asp Thr Tyr Ile Glu Glu Ala			
180	185	190	

Glu Lys Tyr Lys Met Gln Leu Gln Glu Gln Phe Asp Asn Leu Asn Ala
 195 200 205

His Glu Thr Ser Lys Leu Glu Ile Glu Ala Ser His Ser Glu Lys Leu
 210 215 220

Glu Leu Leu Lys Lys Ala Tyr Glu Ala Ser Leu Ser Glu Ile Lys Lys
 225 230 235 240

Gly His Glu Ile Glu Lys Lys Ser Leu Glu Asp Leu Leu Ser Glu Lys
 245 250 255

Gln Glu Ser Leu Glu Lys Gln Ile Asn Asp Leu Lys Ser Glu Asn Asp
 260 265 270

Ala Leu Asn Glu Lys Leu Lys Ser Glu Glu Gln Lys Arg Arg Ala Arg
 275 280 285

Glu Lys Ala Asn Leu Lys Asn Pro Gln Ile Met Tyr Leu Glu Gln Glu
 290 295 300

Leu Glu Ser Leu Lys Ala Val Leu Glu Ile Lys Asn Glu Lys Leu His
 305 310 315 320

Gln Gln Asp Ile Lys Leu Met Lys Met Glu Lys Leu Val Asp Asn Asn
 325 330 335

Thr Ala Leu Val Asp Lys Leu Lys Arg Phe Gln Gln Glu Asn Glu Glu
 340 345 350

Leu Lys Ala Arg Met Asp Lys His Met Ala Ile Ser Arg Gln Leu Ser
 355 360 365

Thr Glu Gln Ala Val Leu Gln Glu Ser Leu Glu Lys Glu Ser Lys Val
 370 375 380

Asn Lys Arg Leu Ser Met Glu Asn Glu Glu Leu Leu Trp Lys Leu His
 385 390 395 400

Asn Gly Asp Leu Cys Ser Pro Lys Arg Ser Pro Thr Ser Ser Ala Ile
 405 410 415

Pro Leu Gln Ser Pro Arg Asn Ser Gly Ser Phe Pro Ser Pro Ser Ile
 420 425 430

Ser Pro Arg *
 435

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGTTGTTGT	CTCCCAAATT	CTCCTTATCC	ACCATTACCA	TACGACTGAC	GGCCAAAGGA	60
TTGCTTCGAA	ACCTTCGACT	TCCTTCAGGG	TTTAGGAGAA	GCACTGTTGT	TTTCCACACA	120
GTTGAAAAGA	GCAGGCAAAA	GAATCCTCGA	AGCTTATGTA	TCCAGCCACA	GACAGCTCCC	180
GATGCGCTGC	CCCCTGAGAA	AACACTTGAA	TTGACGCAAT	ATAAAACAAA	ATGTGAAAAC	240
CAAAGTGGAT	TTATCCTGCA	GCTCAAGCAG	CTTCTTGCTC	GTGGTAATAC	CAAGTTGAG	300
GCATTGACAG	TTGTGATTCA	GCACCTGCTG	TCTGAGCGGG	AGGAAGCAGT	GAAACAACAC	360
AAAACCTAT	CTCAAGAACT	TGTTAACCTC	CGGGGAGAGC	TAGTCACTGC	TTCAACCACC	420
TGTGAGAAAT	TAGAAAAAGC	CAGGAATGAG	TTACAAACAG	TGTATGAAGC	ATTCGTCCAG	480
CAGCACCAAGG	CTGAAAAAAC	AGAACGAGAG	AATCGGCTTA	AAGAGTTTA	CACCAGGGAG	540
TATGAAAAGC	TTCGGGACAC	TTACATTGAA	GAAGCAGAGA	AGTACAAAAT	GCAATTGCAA	600
GAGCAGTTG	ACAACTTAAA	TGCGCATGAA	ACCTCTAAGT	TGGAAATTGA	AGCTAGCCAC	660
TCAGAGAAAC	TTGAATTGCT	AAAGAAGGCC	TATGAAGCCT	CCCTTCAGA	AATTAAGAAA	720
GGCCATGAAA	TAGAAAAGAA	ATCGCTTGAA	GATTTACTTT	CTGAGAAGCA	GGAATCGCTA	780
GAGAAGCAAA	TCAATGATCT	GAAGAGTGAA	AATGATGCTT	TAAATGAAAA	ATTGAAATCA	840
GAAGAACAAA	AAAGAAGAGC	AAGAGAAAAAA	GCAAATTGAA	AAAATCCTCA	GATCATGTAT	900
CTAGAACAGG	AGTTAGAAAAG	CCTGAAAGCT	GTGTTAGAGA	TCAAGAATGA	GAAACTGCAT	960
CAACAGGACA	TCAAGTTAAT	AAAAATGGAG	AAACTGGTGG	ACAACAAACAC	AGCATTGGTT	1020
GACAAATTGA	AGCGTTCCA	GCAGGAGAAT	GAAGAATTGA	AAGCTCGGAT	GGACAAGCAC	1080
ATGGCAATCT	CAAGGCAGCT	TTCCACGGAG	CAGGCTGTT	TGCAAGAGTC	GCTGGAGAAG	1140
GAGTCGAAAG	TCAACAAAGCG	ACTCTCTATG	GAAAACGAGG	AGCTTCTGTG	GAAACTGCAC	1200
AATGGGGACC	TGTGTAGCCC	CAAGAGATCC	CCCACATCCT	CCGCCATCCC	TTTGCAGTCA	1260
CCAAGGAATT	CGGGCTCCTT	CCCTAGCCCC	AGCATTTCAC	CCAGATGA		1308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

18

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CAAGCGTTCT CTCGGAGGAC A

21

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGCGGATCCC AGACAGACCG GACGGAACTG GAG

33

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCGGAATTCA CTACAACCTT TCGTTTAAAG CATC

34